



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,758A

DATE: 06/04/2002

TIME: 16:03:52

Input Set : A:\46355862.app

Output Set: N:\CRF3\06042002\I831758A.raw

P6
ENTERED

3 <110> APPLICANT: WATANABE, TAKUYA
 4 KIKUCHI, KUNIKO
 5 TERAOKA, YASUKO
 6 SHINTANI, YASUSHI
 7 HINUMA, SHUJI
 8 FUKUSUMI, SHOJI
 9 FUJII, RYO
 10 HOSOYA, MASAKI
 11 KITADA, CHIEKO
 13 <120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN, ITS DNA AND
 14 LIGAND THEREOF
 16 <130> FILE REFERENCE: 46342-55862
 18 <140> CURRENT APPLICATION NUMBER: 09/831,758A
 C--> 19 <141> CURRENT FILING DATE: 2002-04-05
 21 <150> PRIOR APPLICATION NUMBER: JP 10-323759
 22 <151> PRIOR FILING DATE: 1998-11-13
 24 <150> PRIOR APPLICATION NUMBER: JP 11-0600030
 25 <151> PRIOR FILING DATE: 1999-03-08
 27 <150> PRIOR APPLICATION NUMBER: JP 11-106812
 28 <151> PRIOR FILING DATE: 1999-04-14
 30 <150> PRIOR APPLICATION NUMBER: JP 11-166672
 31 <151> PRIOR FILING DATE: 1999-06-14
 33 <150> PRIOR APPLICATION NUMBER: JP 11-221640
 34 <151> PRIOR FILING DATE: 1999-08-04
 36 <150> PRIOR APPLICATION NUMBER: JP 11-259818
 37 <151> PRIOR FILING DATE: 1999-09-14
 39 <160> NUMBER OF SEQ ID NOS: 63
 41 <170> SOFTWARE: PatentIn Ver. 2.1
 43 <210> SEQ ID NO: 1
 44 <211> LENGTH: 180
 45 <212> TYPE: PRT
 46 <213> ORGANISM: Homo sapiens
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 52 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met
 53 20 25 30
 55 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
 56 35 40 45
 58 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp
 59 50 55 60
 61 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys
 62 65 70 75 80

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64 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val
65                               85                               90                               95
67 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser
68                               100                              105                              110
70 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro
71                               115                              120                              125
73 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu
74                               130                              135                              140
76 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
77 145                               150                              155                              160
79 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
80                               165                              170                              175
82 Lys Gln Ser Arg
83                               180
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89 <213> ORGANISM: Homo sapiens
91 <220> FEATURE:
92 <221> NAME/KEY: CDS
93 <222> LOCATION: (1)..(540)
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98 1 5 10 15
100 tca agc ttg tta aca tca aac att ttt tgt gca gat gaa tta gtg atg 96
101 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met
102 20 25 30
104 tcc aat ctt cac agc aaa gaa aat tat gac aaa tat tct gag cct aga 144
105 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
106 35 40 45
108 gga tac cca aaa ggg gaa aga agc ctc aat ttt gag gaa tta aaa gat 192
109 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp
110 50 55 60
112 tgg gga cca aaa aat gtt att aag atg agt aca cct gca gtc aat aaa 240
113 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys
114 65 70 75 80
116 atg cca cac tcc ttc gcc aac ttg cca ttg aga ttt ggg agg aac gtt 288
117 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val
118 85 90 95
120 caa gaa gaa aga agt gct gga gca aca gcc aac ctg cct ctg aga tct 336
121 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser
122 100 105 110
124 gga aga aat atg gag gtg agc ctc gtg aga cgt gtt cct aac ctg ccc 384
125 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro
126 115 120 125
128 caa agg ttt ggg aga aca aca aca gcc aaa agt gtc tgc agg atg ctg 432
129 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu
130 130 135 140

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132 agt gat ttg tgt caa gga tcc atg cat tca cca tgt gcc aat gac tta 480
133 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
134 145 150 155 160
136 ttt tac tcc atg acc tgc cag cac caa gaa atc cag aat ccc gat caa 528
137 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
138 165 170 175
140 aaa cag tca agg taa 543
141 Lys Gln Ser Arg
142 180
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148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
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153 <400> SEQUENCE: 3
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158 <211> LENGTH: 27
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial Sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
165 <400> SEQUENCE: 4
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169 <210> SEQ ID NO: 5
170 <211> LENGTH: 30
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
177 <400> SEQUENCE: 5
178 gcacatagag acttaatttt agatttagac 30
181 <210> SEQ ID NO: 6
182 <211> LENGTH: 27
183 <212> TYPE: DNA
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187 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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194 <211> LENGTH: 27
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
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202 cagctttagg gacaggctcc aggtttc 27

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Input Set : A:\46355862.app

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205 <210> SEQ ID NO: 8
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208 <213> ORGANISM: Homo sapiens
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214 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met
215           20           25           30
217 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
218           35           40           45
220 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp
221           50           55           60
223 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys
224   65           70           75           80
226 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val
227           85           90           95
229 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser
230           100          105          110
232 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro
233           115          120          125
235 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu
236           130          135          140
238 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
239 145          150          155          160
241 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
242           165          170          175
244 Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu
245           180          185          190
247 Lys Gln Glu Lys
248           195
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252 <211> LENGTH: 591
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254 <213> ORGANISM: Homo sapiens
256 <220> FEATURE:
257 <221> NAME/KEY: CDS
258 <222> LOCATION: (1)..(588)
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262 Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr
263   1           5           10           15
265 tca agc ttg tta aca tca aac att ttt tgt gca gat gaa tta gtg atg   96
266 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met
267           20           25           30
269 tcc aat ctt cac agc aaa gaa aat tat gac aaa tat tct gag cct aga  144
270 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
271           35           40           45
273 gga tac cca aaa ggg gaa aga agc ctc aat ttt gag gaa tta aaa gat  192

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274 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp
275      50      55      60
277 tgg gga cca aaa aat gtt att aag atg agt aca cct gca gtc aat aaa 240
278 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys
279 65      70      75      80
281 atg cca cac tcc ttc gcc aac ttg cca ttg aga ttt ggg agg aac gtt 288
282 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val
283      85      90      95
285 caa gaa gaa aga agt gct gga gca aca gcc aac ctg cct ctg aga tct 336
286 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser
287      100      105      110
289 gga aga aat atg gag gtg agc ctc gtg aga cgt gtt cct aac ctg ccc 384
290 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro
291      115      120      125
293 caa agg ttt ggg aga aca aca aca gcc aaa agt gtc tgc agg atg ctg 432
294 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu
295      130      135      140
297 agt gat ttg tgt caa gga tcc atg cat tca cca tgt gcc aat gac tta 480
298 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
299 145      150      155      160
301 ttt tac tcc atg acc tgc cag cac caa gaa atc cag aat ccc gat caa 528
302 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
303      165      170      175
305 aaa cag tca agg aga ctg cta ttc aag aaa ata gat gat gca gaa ttg 576
306 Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu
307      180      185      190
309 aaa caa gaa aaa taa 591
310 Lys Gln Glu Lys
311      195
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317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
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327 <211> LENGTH: 27
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
334 <400> SEQUENCE: 11
335 gggaggaaca tggaagaaga aaggagc 27
338 <210> SEQ ID NO: 12
339 <211> LENGTH: 27
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; N Pos. 3,9
Seq#:21; N Pos. 3,9,12
Seq#:22; N Pos. 3,6,9
Seq#:23; N Pos. 3,6,9,12
Seq#:24; N Pos. 3,6,9
Seq#:25; N Pos. 3,6,9,12